WHAT IS CLAIMED IS:

1. An isolated nucleic acid comprising a genomic, complementary or composite polynucleotide sequence encoding a polypeptide having an invertase activity in an apoplastic environment and an N terminal amino acid sequence serving for secretion into an apoplast.

2. The isolated nucleic acid of claim 1, wherein said polypeptide is at least 80 % homologous to SEQ ID NO:5 as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap creation penalty equals 8 and gap extension penalty equals 2.

3. The isolated nucleic acid of claim 1, wherein said polynucleotide is hybridizable with SEQ ID NOs:1, 4 or 6 under hybridization conditions of hybridization solution containing 10 % dextrane sulfate, 1 M NaCl, 1 % SDS and 5 x 10^6 cpm ^{32}p labeled probe, at 65 °C, with a final wash solution of 0.1 x SSC and 0.1 % SDS and final wash at 60 °C.

4. The isolated nucleic acid of claim 1, wherein said polynucleotide is at least 80 % identical with SEQ ID NO:6 as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap weight equals 50, length weight equals 3, average match equals 10 and average mismatch equals -9.

5. The isolated nucleic acid of claim 1, wherein said polypeptide is as set forth in SEQ ID NO:5 or portions thereof.

6. The isolated nucleic acid of claim 1, wherein said polynucleotide is as set forth in SEQ ID NO:6 or portions thereof.

7. An isolated nucleic acid comprising a genomic, complementary or composite polynucleotide sequence encoding a polypeptide having an invertase activity, said polypeptide is at least 80 % homologous to SEQ ID NO:5 as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap creation penalty equals 8 and gap extension penalty equals 2.

8. The isolated nucleic acid of claim 7, wherein said polynucleotide is hybridizable with SEQ ID NOs:1, 4 or 6 under hybridization conditions of hybridization solution containing 10 % dextrane sulfate, 1 M NaCl, 1 % SDS and 5 x 10^6 cpm ^{32}p labeled probe, at 65 °C, with a final wash solution of 0.1 x SSC and 0.1 % SDS and final wash at 60 °C.

9. The isolated nucleic acid of claim 7, wherein said polynucleotide is at least 80 % identical with SEQ ID NO:6 as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap weight equals 50, length weight equals 3, average match equals 10 and average mismatch equals -9.

10. The isolated nucleic acid of claim 7, wherein said polypeptide is as set forth in SEQ ID NO:5 or portions thereof.

11. The isolated nucleic acid of claim 7, wherein said polynucleotide is as set forth in SEQ ID NO:6 or portions thereof.

12. A nucleic acid construct comprising the isolated nucleic acid of claim 1.

13. The nucleic acid construct of claim 12, further comprising a promoter for regulating expression of the isolated nucleic acid in an orientation selected from the group consisting of sense and antisense orientation.

14. The nucleic acid construct of claim 12, further comprising a positive and a negative selection markers for selecting for homologous recombination events.

15. A plant cell, tissue or a whole plant comprising the nucleic acid construct of claim 12.

16. A nucleic acid construct comprising the isolated nucleic acid of claim 7.

17. The nucleic acid construct of claim 16, further comprising a promoter for regulating expression of the isolated nucleic acid in an orientation selected from the group consisting of sense and antisense orientation.

18. The nucleic acid construct of claim 16, further comprising a positive and a negative selection markers for selecting for homologous recombination events.

19. A plant cell, tissue or a whole plant comprising the nucleic acid construct of claim 16.

20. An isolated nucleic acid comprising a genomic, complementary or composite polynucleotide sequence hybridizable with SEQ ID NOs:1, 4 or 6

under hybridization conditions of hybridization solution containing 10 % dextrane sulfate, 1 M NaCl, 1 % SDS and 5 x 10^6 cpm ^{32}p labeled probe, at 65 °C, with a final wash solution of 0.1 x SSC and 0.1 % SDS and final wash at 60 °C.

21. An isolated nucleic acid comprising a genomic, complementary or composite polynucleotide sequence at least 80 % identical with SEQ ID NOs:1, 4 or 6 as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap weight equals 50, length weight equals 3, average match equals 10 and average mismatch equals -9

22. An isolated nucleic acid comprising a polynucleotide sequence as set forth in SEQ ID NOs:1, 4 or 6.

23. An isolated nucleic acid comprising a polynucleotide sequence encoding a polypeptide as set forth in SEQ ID NO:5.

24. A recombinant protein comprising a polypeptide having an invertase activity in an apoplastic environment and an N terminal amino acid sequence serving for secretion into an apoplast.

25. The recombinant protein of claim 24, wherein said polypeptide is at least 80 % homologous to SEQ ID NO:5, as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap creation penalty equals 8 and gap extension penalty equals 2.

26. The recombinant protein of claim 24, wherein said polypeptide includes at least a portion of SEQ ID NO:5.

27. The recombinant protein of claim 24, wherein the protein is encoded by a polynucleotide hybridizable with SEQ ID NOs:1, 4 or 6 or a portion thereof under hybridization conditions of hybridization solution containing 10 % dextrane sulfate, 1 M NaCl, 1 % SDS and 5 x 10^6 cpm ^{32}p labeled probe, at 65 °C, with a final wash solution of 0.1 x SSC and 0.1 % SDS and final wash at 60 °C.

28. The recombinant protein of claim 24, wherein the protein is encoded by a polynucleotide at least 80 % identical with SEQ ID NO:6 or portions thereof as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap weight equals 50, length weight equals 3, average match equals 10 and average mismatch equals -9.

29. A recombinant protein comprising a polypeptide as set forth in SEQ ID NO:5.

30. A recombinant protein comprising a polypeptide at least 80 % homologous to SEQ ID NO:5 as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap creation penalty equals 8 and gap extension penalty equals 2.

31. A method of increasing a level of a monosaccharide in a plant tissue, the method comprising the step of expressing in the plant tissue a polypeptide having invertase activity, wherein said polypeptide is at least 80 % homologous to SEQ ID NO:5 as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman

algorithm, where gap creation penalty equals 8 and gap extension penalty equals 2.

32. A method of increasing a level of a monosaccharide in a plant tissue, the method comprising the step of expressing a polypeptide having invertase activity, wherein said polypeptide is encoded by a polynucleotide hybridizable with SEQ ID NOs:1, 4 or 6 or a portion thereof under hybridization conditions of hybridization solution containing 10 % dextrane sulfate, 1 M NaCl, 1 % SDS and 5 x 10^6 cpm ^{32}p labeled probe, at 65 °C, with a final wash solution of 0.1 x SSC and 0.1 % SDS and final wash at 60 °C.

33. A method of increasing a level of a monosaccharide in a plant tissue, the method comprising the step of expressing a polypeptide having invertase activity, wherein said polypeptide is encoded by a polynucleotide at least 80 % identical with SEQ ID NO:6 as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap weight equals 50, length weight equals 3, average match equals 10 and average mismatch equals -9.